

AMENDMENTS

IN THE SPECIFICATION:

Please amend the specification at page 27, line 10 as follows:

Raw data obtained from hybridization experiments was analyzed using bioinformatics tools to identify signals associated with differential gene expression. Basic statistical methods such as t-test with a p value < 0.05 and fold change ≥ 1.5 were performed by Affymetrix® Data Mining Tool 3.0. Differential gene expression results were combined in a Venn Diagram approach to find common sets of genes found from multiple methods. Hierarchical clustering was also used, where a distance matrix was first calculated, containing the distances between every pair of specimens in the data set. A tree was then built by merging the two closest specimens until all of the specimens were contained in the tree. Hierarchical Cluster Analysis was performed using either Cluster and TrecView Software (<http://rana.lbl.gov/EisenSoftware.htm>) or GeneSpring (Silicon Genetics).